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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/506,079H

DATE: 04/27/2004
 TIME: 09:52:36

Input Set : A:\49321-16.ST25.txt
 Output Set: N:\CRF4\04272004\I506079H.raw

3 <110> APPLICANT: Clinton, Gail M.
 4 Evans, Adam
 5 Henner, William D.
 7 <120> TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
 9 <130> FILE REFERENCE: 49321-16
 11 <140> CURRENT APPLICATION NUMBER: US 09/506,079H
 12 <141> CURRENT FILING DATE: 2000-02-16
 14 <160> NUMBER OF SEQ ID NOS: 15
 16 <170> SOFTWARE: PatentIn version 3.2
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 79
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: MISC_FEATURE
 26 <222> LOCATION: (2)..(2)
 27 <223> OTHER INFORMATION: Applicants herein disclose Thr and Ser sequence variants at
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 28 position
 30 <220> FEATURE:
 31 <221> NAME/KEY: MISC_FEATURE
 32 <222> LOCATION: (5)..(5)
 33 <223> OTHER INFORMATION: Applicants herein disclose Leu and Pro sequence variants at
 this
 34 position
 36 <220> FEATURE:
 37 <221> NAME/KEY: MISC_FEATURE
 38 <222> LOCATION: (6)..(6)
 39 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at
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 40 position
 42 <220> FEATURE:
 43 <221> NAME/KEY: MISC_FEATURE
 44 <222> LOCATION: (16)..(16)
 45 <223> OTHER INFORMATION: Applicants herein disclose Leu and Gln sequence variants at
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 46 position
 48 <220> FEATURE:
 49 <221> NAME/KEY: MISC_FEATURE
 50 <222> LOCATION: (18)..(18)
 51 <223> OTHER INFORMATION: Applicants herein disclose Met and Leu sequence variants at
 this
 52 position
 54 <220> FEATURE:

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55 <221> NAME/KEY: MISC_FEATURE
56 <222> LOCATION: (21)..(21)
57 <223> OTHER INFORMATION: Applicants herein disclose Gly, Asp, Ala and Val sequence
58 variants at this position

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60 <220> FEATURE:
 61 <221> NAME/KEY: MISC_FEATURE
 62 <222> LOCATION: (36)..(36)
 63 <223> OTHER INFORMATION: Applicants herein disclose Leu and Ile sequence variants at this
 64 position
 66 <220> FEATURE:
 67 <221> NAME/KEY: MISC_FEATURE
 68 <222> LOCATION: (54)..(54)
 69 <223> OTHER INFORMATION: Applicants herein disclose Pro and Arg sequence variants at this
 70 position
 72 <220> FEATURE:
 73 <221> NAME/KEY: MISC_FEATURE
 74 <222> LOCATION: (64)..(64)
 75 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at this
 76 position
 78 <220> FEATURE:
 79 <221> NAME/KEY: MISC_FEATURE
 80 <222> LOCATION: (73)..(73)
 81 <223> OTHER INFORMATION: Applicants herein disclose Asp and Asn sequence variants at this
 82 position
 84 <400> SEQUENCE: 1
 W--> 86 Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro Xaa
 87 1 5 10 15
 90 Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro
 91 20 25 30
 94 Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu
 95 35 40 45
 98 Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val Gly Arg Gly Xaa
 99 50 55 60
 102 Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg Tyr Glu Gly
 103 65 70 75
 106 <210> SEQ ID NO: 2
 107 <211> LENGTH: 419
 108 <212> TYPE: PRT
 109 <213> ORGANISM: Homo sapiens
 112 <220> FEATURE:
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 114 <222> LOCATION: (342)..(342)
 115 <223> OTHER INFORMATION: Applicants herein disclose Thr and Ser sequence variants at this
 116 position
 118 <220> FEATURE:
 119 <221> NAME/KEY: MISC_FEATURE
 120 <222> LOCATION: (345)..(345)
 121 <223> OTHER INFORMATION: Applicants herein disclose Leu and Pro sequence variants at this
 122 position
 124 <220> FEATURE:
 125 <221> NAME/KEY: MISC_FEATURE

126 <222> LOCATION: (346)..(346)

127 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at
this

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128 position
 130 <220> FEATURE:
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 132 <222> LOCATION: (356)..(356)
 133 <223> OTHER INFORMATION: Applicants herein disclose Leu and Gln sequence variants at this
 134 position
 136 <220> FEATURE:
 137 <221> NAME/KEY: MISC_FEATURE
 138 <222> LOCATION: (358)..(358)
 139 <223> OTHER INFORMATION: Applicants herein disclose Met and Leu sequence variants at this
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 142 <220> FEATURE:
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 144 <222> LOCATION: (361)..(361)
 145 <223> OTHER INFORMATION: Applicants herein disclose Gly, Asp, Ala and Val sequence variants at this position
 148 <220> FEATURE:
 149 <221> NAME/KEY: MISC_FEATURE
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 154 <220> FEATURE:
 155 <221> NAME/KEY: MISC_FEATURE
 156 <222> LOCATION: (394)..(394)
 157 <223> OTHER INFORMATION: Applicants herein disclose Pro and Arg sequence variants at this
 158 position
 160 <220> FEATURE:
 161 <221> NAME/KEY: MISC_FEATURE
 162 <222> LOCATION: (404)..(404)
 163 <223> OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at this
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 166 <220> FEATURE:
 167 <221> NAME/KEY: MISC_FEATURE
 168 <222> LOCATION: (413)..(413)
 169 <223> OTHER INFORMATION: Applicants herein disclose Asp and Asn sequence variants at this
 170 position
 172 <400> SEQUENCE: 2
 174 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Ala Leu Leu
 175 1 5 10 15
 178 Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
 179 20 25 30
 182 Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
 183 35 40 45
 186 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
 187 50 55 60
 190 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
 191 65 70 75 80

194 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
195 85 90 95

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198 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
 199 100 105 110
 202 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
 203 115 120 125
 206 Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
 207 130 135 140
 210 Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
 211 145 150 155 160
 214 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
 215 165 170 175
 218 Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
 219 180 185 190
 222 His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
 223 195 200 205
 226 Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
 227 210 215 220
 230 Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
 231 225 230 235 240
 234 Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
 235 245 250 255
 238 His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
 239 260 265 270
 242 Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
 243 275 280 285
 246 Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
 247 290 295 300
 250 Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
 251 305 310 315 320
 254 Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
 255 325 330 335
 W--> 258 Pro Cys Ala Arg Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val
 259 340 345 350
 262 Pro Val Pro Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser
 263 355 360 365
 266 Phe Leu Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro
 267 370 375 380
 270 Leu Ala Pro Leu Asp Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val
 271 385 390 395 400
 274 Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg
 275 405 410 415
 278 Tyr Glu Gly
 282 <210> SEQ ID NO: 3
 283 <211> LENGTH: 19
 284 <212> TYPE: DNA
 285 <213> ORGANISM: Artificial Sequence
 287 <220> FEATURE:
 288 <223> OTHER INFORMATION: HER-2-specific oligonucleotide primer
 290 <400> SEQUENCE: 3
 291 tgagcaccat ggagctggc

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294 <210> SEQ ID NO: 4
295 <211> LENGTH: 22
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: HER-2-specific oligonucleotide primer
302 <400> SEQUENCE: 4
303 tccggcagaa atgccaggct cc 22
306 <210> SEQ ID NO: 5
307 <211> LENGTH: 22
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: HER-2 cDNA-specific oligonucleotide primer
314 <400> SEQUENCE: 5
315 aacacacgcgg tgtgagaagt gc 22
318 <210> SEQ ID NO: 6
319 <211> LENGTH: 21
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: HER-2 ECDIIIA-region-specific oligonucleotide primer
326 <400> SEQUENCE: 6
327 ataccgggac aggtcaacag c 21
330 <210> SEQ ID NO: 7
331 <211> LENGTH: 20
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: HER-2 ECDIIIA-region-specific oligonucleotide primer
338 <400> SEQUENCE: 7
339 tctgggtacc cactcaactgc 20
342 <210> SEQ ID NO: 8
343 <211> LENGTH: 22
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
348 <223> OTHER INFORMATION: HER-2 exon-specific oligonucleotide primer
350 <400> SEQUENCE: 8
351 ttcacactgg cacgtccaga cc 22
354 <210> SEQ ID NO: 9
355 <211> LENGTH: 27
356 <212> TYPE: DNA
357 <213> ORGANISM: Artificial Sequence
359 <220> FEATURE:
360 <223> OTHER INFORMATION: HER-2 cDNA-specific oligonucleotide primer
362 <400> SEQUENCE: 9
363 gcacggatcc atagcagact gaggagg 27
366 <210> SEQ ID NO: 10
  
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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,5,6,16,18,21,36,54,64,73

Seq#:2; Xaa Pos. 342,345,346,356,358,361,376,394,404,413

Seq#:10; N Pos. 62

Seq#:10; Xaa Pos. 2,5,6,16,18,21,36,54,64,73

VERIFICATION SUMMARY
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Input Set : A:\49321-16.ST25.txt
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L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
M:341 Repeated in SeqNo=1
L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:336
M:341 Repeated in SeqNo=2
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:48
M:341 Repeated in SeqNo=10